DATE: Wednesday, October 29, 2003   Printable Copy   Create Case

Set Name	**Query**	**Hit Count**	**Set Name**
side by side			result set

DB=; PLUR=YES; OP=ADJ

L6	'alpha d' same (antibod$) and (antibod$) same (inhibit$ or suppress$ or block$ or modulat$) same (tnf$ or tumor adj necrosis or tumour adj necrosis)	6	L6
L5	'alpha d' same (inhibit$ or suppress$ or block$ or modulat$) same (tnf$ or tumor adj necrosis or tumour adj necrosis)	12	L5
L4	'alpha d' and (tnf$ or tumor adj necrosis or tumour adj necrosis)	631	L4
L3	L1 and 'alpha d'	16	L3

DB=USPT,PGPB; PLUR=YES; OP=ADJ

| L2 | L1 and alphad | 1 | L2 |
| L1 | gallatin.in. | 73 | L1 |

END OF SEARCH HISTORY

WEST

End of Result Set

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L3: Entry 1 of 1   File: USPT   Jun 26, 2001

US-PAT-NO: 6251395
DOCUMENT-IDENTIFIER: US 6251395 B1
** See image for Certificate of Correction **

TITLE: Methods of inhibiting inflammation at the site of a central nervous system injury with alphaD-specific antibodies

DATE-ISSUED: June 26, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Gallatin; W. Michael	Mercer Island	WA	98040	
Van der Vieren; Monica	Seattle	WA	98107	

US-CL-CURRENT: 424/144.1; 424/130.1, 424/141.1, 424/143.1, 424/153.1, 424/154.1, 424/173.1, 530/387.1, 530/388.1, 530/388.2, 530/388.22, 530/388.7, 530/388.73, 530/388.75

CLAIMS:

What is claimed is:

1. A method for inhibiting macrophage infiltration at the site of a central nervous system injury comprising the step of administering to an individual an effective amount of an anti-.alpha..sub.d monoclonal antibody.

2. The method according to claim 1 wherein the anti-.alpha..sub.d monoclonal antibody blocks binding between .alpha..sub.d and a binding partner.

3. The method according to claim 2 wherein the binding partner is VCAM-1.

4. The method according to claim 1 where the anti-.alpha..sub.d monoclonal antibody is selected from the group consisting of the monoclonal antibody secreted by hybridoma 226H (ATCC Accession No: HB-12592) and the monoclonal antibody secreted by hybridoma 236L (ATCC Accession No: HB-12593).

5. The method according to any one of claims 1 through 4 wherein the central nervous system injury is a spinal cord injury.

6. A method for reducing inflammation at the site of a central nervous system injury comprising the step of administering to an individual an effective amount of an anti-.alpha..sub.d monoclonal antibody.

7. The method according to claim 6 wherein the anti-.alpha..sub.d monoclonal antibody blocks binding between .alpha..sub.d and a binding partner.

8. The method according to claim 7 wherein the binding partner is VCAM-1.

9. The method according to claim 6 where the anti-.alpha..sub.d monoclonal antibody is selected from the group consisting of the monoclonal antibody secreted by hybridoma 226H (ATCC Accession No: HB-12592) and the monoclonal antibody secreted by hybridoma 236L (ATCC Accession No: HB-12593).

WEST

Generate Collection   Print

L2: Entry 2 of 14   File: USPT   Aug 13, 2002

US-PAT-NO: 6432404
DOCUMENT-IDENTIFIER: US 6432404 B1

TITLE: Methods of inhibiting locomotor damage following spinal cord injury with
.alpha. D-specific antibodies

DATE-ISSUED: August 13, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Gallatin; W. Michael	Mercer Island	WA		
Van der Vieren; Monica	Snohomish	WA		

US-CL-CURRENT: 424/144.1; 424/130.1, 424/141.1, 424/143.1, 424/153.1, 424/154.1,
424/173.1, 530/387.1, 530/388.1, 530/388.2, 530/388.22, 530/388.7, 530/388.73,
530/388.75

CLAIMS:

What is claimed is:

1. A method for promoting locomotor recovery following spinal cord injury
comprising the step of administering to a spinal cord injury victim an effective
amount of an anti-.alpha..sub.d monoclonal antibody.

2. A method for inhibiting locomotor damage following spinal cord injury
comprising the step of administering to a spinal cord injury victim an effective
amount of an anti-.alpha..sub.d monoclonal antibody.

3. A method of limiting locomotor impairment following spinal cord injury
comprising the step of administering to a spinal cord injury victim an effective
amount of an anti-.alpha..sub.d monoclonal antibody.

4. A method of limiting autonomic and sensory dysfunction following spinal cord
injury comprising the step of administering to a spinal cord injury victim an
effective amount of an anti-.alpha..sub.d monoclonal antibody.

5. The method of any one of claims 1, 2, 3, or 4 wherein the anti-.alpha..sub.d
monoclonal antibody is secreted by a hybridoma selected from the group consisting
of 217L (ATCC Accession No: HB12701) and 226H (ATCC Accession No: 12502).

6. The method of any one of claims 1, 2, 3, or 4 wherein the anti-.alpha..sub.d
monoclonal antibody competes with 217L (ATCC Accession No: HB 12701) or 226H (ATCC
Accession No: 12502) for binding to .alpha..sub.d.

7. The method of any one of claims 1, 2, 3, or 4 wherein the anti-.alpha..sub.d
monoclonal antibody inhibits .alpha..sub.d binding to an .alpha..sub.d ligand.

8. The method according to any one of claims 1, 2, 3, or 4 wherein the spinal cord
injury comprises compression to the spinal cord.

9. The method of claim 7 wherein the .alpha..sub.d ligand is selected from the
group consisting of ICAM-R and VCAM-1.

10. The method according to any one of claims 6 through 9 wherein the central nervous system injury is a spinal cord injury.

STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number

TO: Phillip Gambel
Location: 8b03 / 9e12
Friday, August 29, 2003
Art Unit: 1644
Phone: 308-3997
Serial Number: 09 / 891943

From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

Jan Delaval
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please perform a sequence and a sequence interference search for

ussn 09 / 891,943   (ifw amd)

SEQ ID NO: 1

SEQ ID NO: 2

thanx

phillip gambel
art unit 1644
308-3997

1644 mailbox 9e12

Jan Delaval
Reference Librarian
. Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
ian.delaval@uspto.gov

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ _____ Examiner __ _____ Date _____

Art Unit _____ Phone Number 30_____ _____ Serial Number _____

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If more than one search is submitted, please prioritize searches in order of need.
****

Please provide a detailed statement of the search topic and describe as specifically as possible the subject matter to be searched Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract

Title of Invention _____ _____ _____ _____

Inventors (please provide full names) ____ _____ _____ ___ ___ _ ___ __ __ _____

_____ __ ___ _____ ___ ___ __ _____

Earliest Priority Filing Date _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number

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Reference Librarian
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CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov

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STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher ____ (av)	NA Sequence (#) ____ ✓	STN ____ ____ ____
Searcher Phone # ____ 4458	AA Sequence (#) ____ ✓	Dialog ____ ____ ____
Search Location ____	Structure (# ____	____ ____ ____
Date Searched ___ 8/26/03	Bibliographic ____	____ ____ ____
Date ___ 8/29/03	Litigation ____	____ ____ ____
Searcher Prep and Search Time ____	Fulltext ____	____ ✓ ____
Online Prep Time ____ 15	Patent Family ____	____ ____ ____
____ +15	Other ____	____ ____ ____
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 16:16:12 ; Search time 17399 Seconds

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(without alignments)
8760.806 Million cell updates/sec

Title:
Perfect score: 3726
Sequence: 1 tgacctcgcactgtgctt............agcataaatttcatatgct 3726

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481336 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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31: em_htg_hum:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_vrt:*
37: em_htg_mam:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	3726	100.0	3726	6	AR052342	AR052342 Sequence
3	3726	100.0	3726	6	AR055140	AR055140 Sequence
4	3726	100.0	3726	6	AR158011	AR158011 Sequence
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7	3726	100.0	3726	6	BD070942	BD070942 Novel hum
8	3726	100.0	3726	6	I13528	I13528 Sequence 1
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ALIGNMENTS

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DEFINITION Sequence 1 from patent US 5817515.
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VERSION   AR044695.1 GI:5966160
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 3726)
AUTHORS   Gallatin,W.Michael. and Van der Vieren,M.
TITLE   Human B2 integrin alpha subunit antibodies
JOURNAL   Patent: US 5817515-A 1 06-OCT-1998;
FEATURES   Location/Qualifiers

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                /organism="unknown"
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ORIGIN

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Best Local Similarity   100.0%;   Pred. No. 0;
Matches 3726;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy    421 CGCCACAGAGTGTCCACATCAAGAGACATGGACAATCGTCTTCCTGATTGACGGCTTCTGGAAGCA 480
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Qy   1381 TCTGCTTCGGTGGATGTTGGACACAGGGGATGGCACAGGCAGGACCTGATCCTCATTGGGGCCTCA 1440
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Db
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: August 28, 2003, 16:12:37 ; Search time 1136 Seconds
(without alignments)
8853.967 Million cell updates/sec

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Perfect score: 3726
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Match Length	DB	DB ID	Description
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2	3726	100.0	3726	18	AAT79220	Human beta 2 integ
3	3726	100.0	3726	19	AAV67281	Human alpha-d enco
4	3726	100.0	3726	19	AAV35236	Human Beta-integri
5	3726	100.0	3726	19	AAV31540	Human beta2 integr
6	3726	100.0	3726	20	AAV08453	Human alpha_d clon
7	3726	100.0	3726	21	AAA60014	Human alpha_d clon
8	3726	100.0	3726	24	ABK82404	Human cDNA encodin

9	3699	99.3	3785	18	AAT79275	Human beta 2 integ
10	3699	99.3	3785	19	AAV67299	Human alpha-d deri
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13	3699	99.3	3785	21	AAA60094	Human alpha-d codi
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23	2315.2	62.1	3803	19	AAV35273	Mouse Beta-integri
24	2315.2	62.1	3803	19	AAV31575	Mouse alpha-d poly
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28	2313.6	62.1	3803	16	AAQ91714	Mouse alpha-d subu
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31	2304.2	61.8	3597	19	AAV35274	Rat beta-integrin
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39	2300.2	61.7	3528	19	AAV63807	Rat alpha-d encodi
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ALIGNMENTS

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XX
DT   28-DEC-1995 (first entry)
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KW   inflammatory bowel disease; asthma; ss.
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OS   Homo sapiens.
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XX
PD   29-JUN-1995.
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PR   05-AUG-1994; 94US-0286889.
PR   23-DEC-1993; 93US-0173497.
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PA   (ICOS-) ICOS CORP.
XX
PI   Gallatin WM, Van Der Vieren M;

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DR   WPI; 1995-246603/31.
DR   P-PSDB; AAR78166.
XX
PS   Claim 1; Page 82-87; 172pp; English.
XX
PT   Alpha sub-unit polypeptide of human beta 2 integrin - used to
PT   identify potential antiinflammatory agents, for the treatment of
PT   graft arteriosclerosis, inflammatory bowel disease, asthma, etc.
XX
CC   A probe based on a partial cDNA clone (given in AAO91727) of canine
CC   alpha-TM1 was used to screen a human spleen cDNA library to identify
CC   clone 19A2 encoding the beta-1 integrin alpha-subunit, alpha-d.
CC   The cDNA was manipulated to allow expression of recombinant alpha-d
CC   subunit in COS and CHO cells.
XX
SQ   Sequence 3726 BP; 817 A; 1064 C; 1054 G; 791 T; 0 other;

Query Match  100.0%;  Score 3726;  DB 16;  Length 3726;
Best Local Similarity  100.0%;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Total number of hits satisfying chosen parameters: 3067400

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	3699	99.3	3785	9	US-09-350-259-98	Sequence 98, Appl
4	3699	99.3	3785	11	US-09-891-943-98	Sequence 98, Appl
5	3583	96.2	3956	9	US-09-350-259-97	Sequence 97, Appl
6	3583	96.2	3956	11	US-09-891-943-97	Sequence 97, Appl
7	2315.2	62.1	3803	9	US-09-350-259-52	Sequence 52, Appl
8	2315.2	62.1	3803	11	US-09-891-943-52	Sequence 52, Appl
9	2304.2	61.8	3597	9	US-09-350-259-54	Sequence 54, Appl
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18	1628.8	43.7	4740	11	US-09-902-481A-2	Sequence 2, Appli
19	1628.8	43.7	4740	14	US-10-207-655-175	Sequence 175, App
20	1484	25.1	1484	9	US-09-350-259-102	Sequence 102, App
21	937	25.1	1484	11	US-09-891-943-102	Sequence 102, App
22	824.4	22.1	1318	9	US-09-350-259-100	Sequence 100, App
23	824.4	22.1	1318	11	US-09-891-943-100	Sequence 100, App
24	624.6	16.8	1006	9	US-09-350-259-24	Sequence 24, Appl
25	624.6	16.8	1006	11	US-09-891-943-24	Sequence 24, Appl
26	494.2	13.3	852	9	US-09-350-259-92	Sequence 92, Appl
27	494.2	13.3	852	11	US-09-891-943-92	Sequence 92, App
28	297.6	8.0	4045	9	US-09-805-517A-37	Sequence 37, Appl
29	280.2	7.5	597	12	US-09-891-943-12	Sequence 12, Appl
30	279.2	7.5	750	14	US-10-066-551-12	Sequence 12, Appl
31	275	7.4	481	11	US-09-102-806-35	Sequence 35, Appl
32	268.2	7.2	670	12	US-09-918-999-6255	Sequence 6255, Ap
33	256.2	6.9	5133	10	US-10-002-631C-196	Sequence 196, App
34	193.8	5.2	3927	12	US-09-945-265-1	Sequence 1, Appli
35	130.6	3.5	2125	9	US-10-177-55-1	Sequence 1, Appli
36	130.6	3.5	2125	14	US-10-125-540-48	Sequence 48, Appl
37	130.6	3.5	4631	11	US-09-984-130-25	Sequence 25, Appl
38	130.6	3.5	4631	12	US-09-836-353A-25	Sequence 25, Appl
39	130.6	3.5	4995	11	US-09-984-130-17	Sequence 17, Appl
40	130.6	3.5	4995	12	US-09-836-353A-17	Sequence 17, Appl
41	115	3.1	501	13	US-10-027-632-141582	Sequence 141582,
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43	67.8	1.8	2100	11	US-09-866-050A-479	Sequence 479, App
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45	67.8	1.8	3380	11	US-09-866-050A-514	Sequence 514, App

ALIGNMENTS

RESULT 1
US-09-350-259-1

; Sequence 1, Application US/09350259
; Patent No. US20020062008A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20020062008A1el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
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; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3726
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(3485)

US-09-350-259-1

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  Best Local Similarity   100.0%;
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Qy   361  AGGGTTCCTGCCTCTTGCCCTGCTGGGCCGGAACAGAGGCCGTGGTCC  420
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Db   361  AGGGTTCCTGCCTCTTGCCCTGCTGGGCCGGAACAGAGGCCGTGGTCC  420

Qy   421  CGGCCAGAGTGTCCACATCAAGAGGATGGAGCATCGTCTTCTCGATTGACGGCTGGTTCTGGAAGCA  480
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Db   421  CGGCCAGAGTGTCCACATCAAGAGGATGGAGCATCGTCTTCTCGATTGACGGCTGGTTCTGGAAGCA  480

Qy   481  TTGACCAAAATGACTTTAACCAGATGAAGGGGCTTTGTCCAAGCTGTCGTCAGTTTG  540
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Db   481  TTGACCAAAATGACTTTAACCAGATGAAGGGGCTTTGTCCAAGCTGTCGTCAGTTTG  540

Qy   541  AGGGCACTGACACCCTGTTTGCACTGATGCAGTACTACTCAAACCTTCACTTCA  600
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Db   541  AGGGCACTGACACCCTGTTTGCACTGATGCAGTACTACTCAAACCTTCACTTCA  600

Qy   601  CCTTCACCCAATTCCCGACCACCCGAGCCACTGGTGGATCCATCGTCTCCCAAC  660
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Db   601  CCTTCACCCAATTCCCGACCACCCGAGCCACTGGTGGATCCATCGTCTCCCAAC  660

Qy   661  TGAAAGGCCTGACGTTCACGGCCACGGGCCATCCTGACGTGCAGCTAGTCGTCATC  720
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Db   661  TGAAAGGCCTGACGTTCACGGCCACGGGCCATCCTGACGTGCAGCTAGTCGTCATC  720

Qy   721  ATAAGAATGGGGCCCGAAAAAAGTGCCAAGAGATCCTCATTGTCATCACAGATGGGCAGA  780
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Db   721  ATAAGAATGGGGCCCGAAAAAAGTGCCAAGAGATCCTCATTGTCATCACAGATGGGCAGA  780

Qy   781  AGTACAAAGACCCCCTGGAATACAGTGATTGCATCCCCAGGAGAGAAGGCTGGCATCA  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  AGTACAAAGACCCCCTGGAATACAGTGATTGCATCCCCAGGAGAGAAGGCTGGCATCA  840

Qy   841  TCCGCTACGCTATCGGGGGTGGACACGGCTTTCCAGGGCACCCGCTTTCCAGGACCTGA  900
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Db   841  TCCGCTACGCTATCGGGGGTGGACACGGCTTTCCAGGGCACCCGCTTTCCAGGACCTGA  900

Qy   901  ATACCATCAGCTCAGCGCCTCCGCAGGACCACGTTGTTCAAGGTGGACAACTTTGCAGCCC  960
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Db   901  ATACCATCAGCTCAGCGCCTCCGCAGGACCACGTTGTTCAAGGTGGACAACTTTGCAGCCC  960

Qy   961  TTGGCCAGCAATCCAGAGAAGGCAGCTGCAGGAGAGTCAGTTGAGGGAACCCAGTCCA  1020
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Qy  1021  GGGCAAGCAGCTCCTTCCAGCACGACAGTGTCCCAAGAAGGCTTCAGCACACCCTCACAA  1080
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Db  1021  GGGCAAGCAGCTCCTTCCAGCACGACAGTGTCCCAAGAAGGCTTCAGCACACCCTCACAA  1080

Qy  1081  TGGATGGGCCTCTTCCTGGGGGCTGTGTGGGGGAGCTTTGCGGTGTCTGAGGGTGCCTTCTGT  1140
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Qy  1141  ATCCCCCAAAATATGAGCCCCCACCTTCATCAACATGTCTCAGGAGGAATGGACTGAGGG  1200
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Qy  1201  ACTCTTACCTGGGTTACTCCACCGAGCTTAGCCCTGGTGGGAAGGGGTACAGAACCTGGTCC  1260
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Db  1201  ACTCTTACCTGGGTTACTCCACCGAGCTTAGCCCTGGTGGGAAGGGGTACAGAACCTGGTCC  1260

Qy  1261  TGGGGGCCCCCGCCTACCCAGCAATACCGGGAAGGCCTGTCATCTTCACCCAGGTGTCCAGGC  1320
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Qy  1441  ATTACTATTGAGCAGAACCCGAGGGGGCCAGGTGTCCGGTTCCGTTGCAGGCTCTAGGGGGCCA  1500
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Qy  1501  GGGTGCAGTGGCCAGTGACGTGTCTCCGGTGGGTGGAGCGGCCACCCCTGGGGCGCGCT  1560
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Db  1501  GGGTGCAGTGGCGAGTGGTGACGGCTGTTCTCCGGTGGGTGGAGCGGCCACCCCTGGGGCGCT  1560

Qy  1561  TTGGGGCAGCCCTGAGTGTTGGGGATGTGAATGTGATGGACAAGGGCAGGGGCTGGCCA  1620
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Qy  1621  TTTGGGGGCCCCCGGGAGAGCAGGAGGAACCGGGGGTTGTCTACTTGTTTCACGGGCCTCAG  1680
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Qy  2041  CAGGTCGTGTTGGACTTCCTGTGCCATTTTCAATGAAACCAAGGACCCACTTTGACTCGAA  2100
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Qy  2221  TCCCCTCCCCCAGAAACCTGGCGTCCTGTGCGTGGGCGTGCACAAGACCTCTTCACTG  2280
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Db  2221  TCCCCTCCCCCAGAAACCTGGCGTCCTGTGCGTGGGCGTGCACAAGACCTCTTCACTG  2280
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: August 28, 2003, 19:08:18 ; Search time 308 seconds
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                                              5339.589 Million cell updates/sec

Title: US-09-891-943-1
Perfect score: 3726
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Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Database :   Issued Patents_NA:*
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                5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	3726	100.0	3726	1	US-08-173-497-1	Sequence 1, Appl
2	3726	100.0	3726	1	US-08-286-889-1	Sequence 1, Appl
3	3726	100.0	3726	1	US-08-485-618-1	Sequence 1, Appl
4	3726	100.0	3726	1	US-08-362-652-1	Sequence 1, Appl
5	3726	100.0	3726	1	US-08-605-672-1	Sequence 1, Appl
6	3726	100.0	3726	1	US-08-482-293A-1	Sequence 1, Appl
7	3726	100.0	3726	1	US-08-943-363-1	Sequence 1, Appl
8	3726	100.0	3726	1	US-09-193-043-1	Sequence 1, Appl
9	3726	100.0	3726	4	US-09-688-307A-1	Sequence 1, Appl
10	3699	99.3	3785	1	US-08-485-618-98	Sequence 98, Appl
11	3699	99.3	3785	1	US-08-605-672-98	Sequence 98, Appl
12	3699	99.3	3785	2	US-08-482-293A-98	Sequence 98, Appl
13	3699	99.3	3785	1	US-08-943-363-98	Sequence 98, Appl
14	3699	99.3	3785	2	US-09-193-043-98	Sequence 98, Appl
15	3699	99.3	3785	4	US-09-688-307A-98	Sequence 98, Appl
16	3583	96.2	3956	1	US-08-485-618-97	Sequence 97, Appl
17	3583	96.2	3956	1	US-08-605-672-97	Sequence 97, Appl
18	3583	96.2	3956	2	US-08-482-293A-97	Sequence 97, Appl
19	3583	96.2	3956	1	US-08-943-363-97	Sequence 97, Appl
20	3583	96.2	3956	2	US-09-193-043-97	Sequence 97, Appl
21	3583	96.2	3956	4	US-09-688-307A-97	Sequence 97, Appl
22	2315.2	62.1	3803	1	US-08-485-618-52	Sequence 52, Appl
23	2315.2	62.1	3803	1	US-08-605-672-52	Sequence 52, Appl
24	2315.2	62.1	3803	2	US-08-362-652-52	Sequence 52, Appl
25	2315.2	62.1	3803	2	US-08-482-293A-52	Sequence 52, Appl
26	2315.2	62.1	3803	2	US-08-943-363-52	Sequence 52, Appl
27	2315.2	62.1	3803	3	US-09-193-043-52	Sequence 52, Appl
28	2315.2	62.1	3803	4	US-09-688-307A-52	Sequence 52, Appl
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32	2304.2	61.8	3597	2	US-08-482-293A-54	Sequence 54, Appl
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35	2300.2	61.8	3597	4	US-09-688-307A-54	Sequence 54, Appl
36	2300.2	61.7	3528	1	US-08-286-889-36	Sequence 36, Appl
37	2300.2	61.7	3528	1	US-08-485-618-36	Sequence 36, Appl
38	2300.2	61.7	3528	1	US-08-362-652-36	Sequence 36, Appl
39	2300.2	61.7	3528	1	US-08-605-672-36	Sequence 36, Appl
40	2300.2	61.7	3528	2	US-08-482-293A-36	Sequence 36, Appl
41	2300.2	61.7	3528	2	US-08-943-363-36	Sequence 36, Appl
42	2300.2	61.7	3528	3	US-09-193-043-36	Sequence 36, Appl
43	2210.8	59.3	3528	4	US-09-688-307A-36	Sequence 36, Appl
44	2210.8	59.3	3519	1	US-08-286-889-45	Sequence 45, Appl
45	2210.8	59.3	3519	1	US-08-173-497-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-173-497-1
Sequence 1, Application US/08173497
; Patent No. 5437958
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van Der Vieren, Monica
; TITLE OF INVENTION: No. 5437958e1 Human 2 Integrin Alpha
; TITLE OF INVENTION: Subunit
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,497
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5437958and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31363
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..3485
US-08-173-497-1

Query Match   100.0%; Score 3726; DB 1; Length 3726;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3726; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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（以下、Qy／Db の核酸配列アラインメントが 1 〜 2220 まで続く。配列データは極めて密で完全な一文字単位での判読は困難。）

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Qy   2161 TGGGGGATGTGGTGAGCCCCATCATTCTGCACTCACTTCTCACTGTGTGAGAGGAGCCCA 2220
Db   2161 GAAAAACCCCTGGGGGACTGGGGGATTCACCTGTGAAAACCCTGAAGCTGCTTTTGCCAGATTGTG 2160
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:　　　　　August 26, 2003, 10:31:43 ; Search time 50 Seconds
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Post-processing: Minimum Match 0%

Title:　　　　US-09-891-943-2
Perfect score: 5987
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Scoring table: BLOSUM62
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Searched:　　283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:　　　283308

Minimum DB length: 0
Maximum DB seq length: 2000000000

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　　　　　　　4: pir4:*

Post-processing: Minimum Match 0%
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　　　　　　　Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length DB	Match	DB ID	Description
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3	3327.5	55.6	1153	2	S00551	leukocyte surface
4	1474	24.6	1170	2	S03308	cell surface glyco
5	1457.5	24.3	1163	2	S56126	lymphocyte fuction
6	1148	19.2	1179	2	A53213	integrin alpha-E c
7	1030.5	17.2	1151	2	A45226	integrin alpha-1 c
8	1030.5	17.2	1180	2	A35854	integrin alpha-1 c
9	1012	16.9	1178	2	S44142	VLA-2 protein homo
10	1007.5	16.8	1170	2	I45914	integrin alpha 2 s
11	1007.5	16.8	1181	2	A33998	integrin alpha-2 c
12	654.5	10.9	1038	2	S06046	integrin alpha-4 c
13	646.5	10.8	1041	2	A41131	lymphocyte-Peyer's
14	638	10.7	1054	2	JC7294	alphaP integrin -
15	611	10.2	1041	2	T31437	integrin alpha cha
16	584.5	9.8	1035	2	I58409	integrin alpha-9 c
17	579.5	9.7	1053	2	I55534	VLA-3 alpha subuni
18	576.5	9.6	1051	2	A35761	cell surface glyco
19	555	9.3	1037	2	A60163	glycoprotein IIb -
20	552	9.2	1049	2	A27079	fibronectin recept
21	548	9.2	1039	2	A34269	integrin alpha-2b
22	547.5	9.1	1051	2	A40021	integrin alpha-3 c
23	535.5	8.9	1053	2	S44250	integrin alpha-3 c
24	534	8.9	1034	2	A36108	integrin alpha-V c
25	524.5	8.8	1394	2	A29937	position-specific
26	497	8.3	1044	2	T10050	integrin alpha-v c
27	496.5	8.3	1072	2	A38457	integrin alpha-6 c
28	493	8.2	1146	2	A27421	integrin alpha-5 c
29	492	8.2	1146	2	S40311	integrin - fruit f
30	477.5	8.0	1044	2	S16516	integrin alpha-8 c
31	473	7.9	1073	2	B36429	integrin alpha-7 c
32	464	7.8	1137	2	JC5950	integrin alpha-7 c
33	462.5	7.7	1091	2	A41543	integrin alpha-6 c
34	446.5	7.5	1045	2	S60571	integrin alpha v c
35	439	7.3	1135	2	I61186	alpha-7 integrin -
36	433.5	7.2	1115	2	T09433	integrin alpha cha
37	431.5	7.2	1115	2	T09403	integrin alpha cha
38	431.5	7.2	1226	2	S44824	F54F2.1 protein -
39	420.5	7.0	1106	2	S38783	integrin alpha cha
40	410.5	6.9	764	2	I36916	glycoprotein IIb -
41	394	6.6	1139	2	S28277	hypothetical prote
42	322.5	5.4	272	2	A55548	integrin alpha-i -
43	319.5	5.3	126	2	B30892	leukocyte adhesior
44	319.5	5.3	1086	2	T18523	integrin alpha cha
45	313.5	5.2	604	2	I36917	glycoprotein IIb -

ALIGNMENTS

RESULT 1
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cell surface glycoprotein CD11c precursor - human
N;Alternate names: leukocyte adhesion receptor p150,95 alpha chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: A36584; A35543; S00864
R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
A;Reference number: A36584
A;Molecule type: DNA
A;Residues: 1-834 <CO2>
A;Note: this sequence has been revised in reference A36584
R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A;Title: CDNA cloning and complete primary structure of the alpha subunit of a leuko
A;Reference number: S00864
A;Accession: S00864
A;Molecule type: mRNA
A;Residues: 1-755; 'L', 757-1163 <CO3>
A;Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Note: part of this sequence was confirmed by protein sequencing
A;Reference number: A35543; MUID:90153906; PMID:2303426
R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
A;Reference number: A36584
A;Contents: erratum
A;Accession: A36584
A;Molecule type: DNA
A;Residues: 1-1163 <COR>
A;Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecu
A;Accession: A35543
A;Genetics:
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 or
C;Cross-references: GDB:119758; OMIM:151510
A;Gene: GDB:ITGAX; CD11C
A;Map position: 16p11.2-16p11.2
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat h
C;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repe
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F;20-1107/Domain: extracellular #status prediced <EXT>
F;149-319/Domain: cell surface glycoprotein CD11c #status predicted <VWA>
F;1108-1133/Domain: transmembrane #status predicted <TMM>
F;1134-1163/Domain: intracellular #status predicted <INT>
F;61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status

Query Match　　63.8%;　　Score 3818;　　DB 1;　　Length 1163;
Best Local Similarity　　65.5%;　　Pred. No. 5.9e-267;
Matches 755;　　Conservative 138;　　Mismatches 253;　　Indels　　6;　　Gaps　　5;

Qy　　　1 TFGTVLLLSVLASYHGFNLDVEEPTIFQEDAGGFGQSVVQFGSRLVVGAPLEVVAANQT 60

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Db     4  TRAALLLFFALATSLGFNLDTEELTAFRVDSAGRGDSVVQYANSWVVVGAPQKITAANQT    63

Qy    61  GRLYDCAAATGMCQPIPLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK   120

Db    64  GGLYQCGYSTGACEPIGLQVPPEAVNMSLGLSLASTTSPSQLLACGPTVHHBCGRNMYLT   123

Qy   121  GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIIDQNDFNQMKGFVQAVMGQFE   180

Db   124  GLGFLLGPT-QLTQRLPVSRQECPRQEQOIVFLIDGSSGISSRNFATMMNFVRAVISOFQ   182

Qy   181  GTDTLFALMQYSNLKLKIHFTTQFRTSPSQQSLVDPIVQLKGLTFTATGILTVVTQLFHH   240

Db   183  RPSTQFSLMQFSNKFQTHFTEEFRRTSNPLISLLASVHOLQGFTYTATAIQNVVHRLFHA   242

Qy   241  KNGARKSARKILIVITDGQKYKDPLEYSDVIFQQAEKAGIIRYAIGVGHAFQGPTARQELN   300

Db   241  SYGARRDATKILIVITDGKEGDSLDYKDVIFADAAGIIRYAIGVGLAFQNRNSWKELN    302

Qy   301  TISSAPPQDHVFKVDNPAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQGFSTALTM   360

Db   303  DIASKPSQEHIFKVEDFDALKDIQNQLKEKIFAIEGTETTSSSSFELEMAQEGFSAVTP   362

Qy   361  DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQNLVL   420

Db   363  DGPVLGAVGSFTWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQSLVL   422

Qy   421  GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILIGAPH   480

Db   423  GAPRYQHTGKAVIFTQVSRQWRMKAEVTGTQIGSYFGASLCSVDVDTDGSTDLVLIGAPH   482

Qy   481  YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI   540

Db   483  YYEQTRGGQVSVCPLPRGWR-RWWCDAVLGYEGQGHPWGRFGAALTVLGDVNGDKLTDVVI   541

Qy   541  GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD   600

Db   542  GAPGEEENRGAVYLFHGVLGPSISPSHSQRIAGSQLSSRLQYFGQALSGGQDLTQDGVD   601

Qy   601  LAVGARGQVLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVLCLTIQXS   660

Db   602  LAVGARGQVLLRTPVILMVGVSMQFIPAEIPRSAFECREQVVSEQTLVQSNICLYIDKR   661

Qy   661  SLDOLG--DIQSSVRFDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLPD   718

Db   662  SKNLLGSRDLQSSVTLDLALDPGRLSPRATFQETKNRSLSRVRVLGLAHICENFNLLPS   721

Qy   719  CVEDVVSIIILIHLNFSLVREPIPSPQNLRPVLAVGSQDLFTASLPFEKNCGQDGLCEGDL   778

Db   722  CVEDSVTPITLRLNFTLVGKPLLAFRNLRPMLAADAQRYFTASLPFEKNCGQADHICQ2NL   781

Qy   779  GVTLSFSGLQTLTVGSSLELNVIVTWNAGEDSYGTVVSLYYPAGLSHRRVSGAQKGPHQ   838

Db   782  GISPSFPGLKSLLVGSNLENAEVMVWNDGEDSYGTTITFSHPAGLSYRYVAEGQKQGQL   841

Qy   839  SALRLACETVPTEDEGLRSSRCSVNHPIPHEGSNGTEIVTFDVSYKATIGDRMLMRASAS   898

Db   842  RSLHLTCDSAPVGSQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVS   901

Qy   899  SENNKASSSKATFCELELPVKYAYYTMISROEESTKYFNFATDEKKMKEAEHRYRVNNLS   958

Db   902  SENNTPRTSKTTFQLELPVKYAVTTVVSSHEQFTKYLNFSESEKESHVAMRYQVNNLG   961

Qy   959  QRDLAISINFWVPVLLNGVAVW-DVVMEAP-SQSLPCVSERKPQHSDFLTQISRSPMLD   1016

Db   962  QRDLPVSINFWVPVELNQEAVAMDVEVSHPQNPSLRCSSEKIAPPASDFLAHIQKNPVLD   1021

Qy  1017  CSIADCLQPRCDVPSFSVVQEELDFTLKGNLSFGWVRETLQKKVLVSVAEIIFDTSVYSQ   1076

Db  1022  CSIAGCLRFRCDVPSFSVQEELDFTLKGNLSFGWVRQILQKKVSVSVAEIIFDTSVYSQ   1081

Qy  1077  LPGQEAFMRAQEMVLEEDEVVNAIPIIMGSSVGALLLALITATLYKLGFFKRHYKEML   1136

Db  1082  LPGQEAFMRAQTTTVLEKYKVHNPTLIVGSSIGGLLLLALITAVLYKVGFFKRQYKEMM   1141

Qy  1137  EDKPEDTATFSG   1148

Db  1142  EEANGQIAPENG   1153
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RESULT 2

RHHU1B

B.

A;Reference number: A31108

A;Molecule type: mRNA

A;Residues: 1-499,501-965,'P',967-1153 <ARN>

A;Cross-references: GB:X76724; NID:g180018; PIDN:AAA58410.1.; PID:g553215

R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.

A;Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence rece

A;Reference number: A32218

A;Molecule type: mRNA

A;Residues: 9-1153 <HIC>

A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

R;Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.

A;Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alph

A;Reference number: A46526

A;Molecule type: DNA

A;Residues: 1-499,501-1153 <FLE>

A;Cross-references: GB:S52227; NID:g263047; PIDN:AAB24821.1; PID:g263049

R;Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:24:48 ; Search time 29 Seconds
                              (without alignments)
                              1882.690 Million cell updates/sec

Title: US-09-891-943-2
Perfect score: 5987
Sequence: 1 TFGTVLLLSVLASYHGFNLD..........DTATFSGDDPSCVAPNVPLS 1161

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5987	100.0	1162	1	Q13349	ITAD_HUMAN	homo sapien
2	3815	63.7	1163	1	Q13349	ITAX_HUMAN	homo sapien
3	3439	57.4	1152	1	P20702	ITAM_HUMAN	homo sapien
4	3327.5	55.6	1153	1	P11215	ITAM_HUMAN	homo sapien
5	1476	24.7	1170	1	P05555	ITAL_HUMAN	homo sapien
6	1457.5	24.3	1163	1	P20701	ITAL_MOUSE	mus musculu
7	1156.5	19.3	1167	1	Q24063	ITAE_MOUSE	mus musculu
8	1156.5	19.2	1167	1	Q60677	ITAE_HUMAN	homo sapien
9	1148	19.1	1179	1	P38570	ITAE_HUMAN	homo sapien
10	1146.5	19.1	1189	1	Q9UKX5	ITAH_HUMAN	homo sapien
11	1131.5	18.9	1167	1	075578	ITAG_HUMAN	homo sapien
12	1030.5	17.2	1151	1	P56199	ITA1_HUMAN	homo sapien
13	1030.5	17.2	1180	1	P18614	ITA1_RAT	rattus norv
14	1012	16.9	1178	1	Q62469	ITA2_MOUSE	mus musculu
15	1007.5	16.8	1170	1	P53710	ITA2_BOVIN	bos taurus
16	1007.5	16.8	1181	1	P17301	ITA2_HUMAN	homo sapien
17	654.5	10.9	1038	1	P13612	ITA4_HUMAN	homo sapien
18	646.5	10.8	1039	1	Q00651	ITA4_MOUSE	mus musculu
19	585.5	9.8	1032	1	Q91687	ITA4_XENLA	xenopus lae
20	584.5	9.8	1035	1	Q13797	ITA9_HUMAN	homo sapien
21	579.5	9.7	1053	1	Q62470	ITA3_MOUSE	mus musculu
22	570.5	9.5	1066	1	P17852	ITA3_CRISP	cricetidae
23	554	9.3	1049	1	P08648	ITA5_HUMAN	homo sapien
24	547	9.1	1039	1	P08514	ITAB_HUMAN	homo sapien
25	540.5	9.0	1066	1	P26006	ITA3_HUMAN	homo sapien
26	538	9.0	1033	1	Q9qum0	ITA5_MOUSE	mus musculu
27	535.5	9.0	1053	1	P11688	ITA5_MOUSE	mus musculu
28	534	8.9	1034	1	Q06274	ITA5_CHICK	gallus gall
29	534	8.9	1050	1	P26008	ITAV_CHICK	gallus gall
30	525.5	8.8	1396	1	Q06274	ITAV_XENLA	xenopus lae
31	497	8.3	1044	1	P12080	ITA2_DROME	drosophila
32	496.5	8.3	1072	1	P43406	ITAV_MOUSE	mus musculu
33	493	8.3	1048	1	P26007	ITA6_CHICK	gallus gall
34	490	8.2	1146	1	P06756	ITA1_DROME	homo sapien
35	486	8.1	1130	1	Q24247	ITA6_HUMAN	drosophila
35	482.5	8.1	1025	1	P23229	ITA8_HUMAN	homo sapien
36	477.5	8.0	1044	1	P53708	ITA8_CHICK	homo sapien
37	455	7.6	1181	1	P26009	ITA7_HUMAN	gallus gall
38	437.5	7.3	1091	1	Q13683	ITA7_HUMAN	homo sapien
39	431.5	7.2	1226	1	Q61739	ITA6_MOUSE	mus musculu
40	430.5	7.2	1179	1	P34446	PAT2_CAEEL	caenorhabdi
41	429.5	7.2	1115	1	Q61739	ITA7_MOUSE	mus musculu
42	420.5	7.0	1106	1	061738	ITA7_MOUSE	mus musculu
43	411.5	6.9	1000	1	044396	ITA3_DROME	drosophila
44	408.5	6.8	1015	1	Q63258	ITA5_DROME	rattus norv
45	394	6.6	1139	1	Q9w1m8	ITA4_DROME	drosophila
					Q9v7a4	ITA1_CAEEL	drosophila
					Q03600	INA1_CAEEL	caenorhabdi

ALIGNMENTS

RESULT 1
ITAD_HUMAN
ID   ITAD_HUMAN   STANDARD;   PRT;   1162 AA.
AC   Q13349; Q15575; Q15576;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Integrin alpha-D precursor (Leukointegrin alpha D) (CD11d) (ADB2).
GN   ITGAD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=96111956; PubMed=8777714;
RA   Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
RA   Staunton D.E., Gallatin W.M.;
RT   "A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
RT   3.";
RL   Immunity 3:683-690(1995).
RN   [2]
RP   SEQUENCE OF 1-235 FROM N.A.
RX   MEDLINE=20187620; PubMed=10722744;
RA   Noti J.D., Johnson A.K., Dillon J.D.;
RT   "Structural and functional characterization of the leukocyte integrin
RT   gene CD11d. Essential role of Sp1 and Sp3.";
RL   J. Biol. Chem. 275:8959-8969(2000).
RN   [3]
RP   SEQUENCE OF 467-537, 571-602, 633-666; 788-834 AND 910-1125 FROM N.A.
RX   MEDLINE=96257236; PubMed=8666289;
RA   Wong D.A., Davis E.M., LeBeau M., Springer T.A.;
RT   "Cloning and chromosomal localization of a novel gene-encoding a human
RT   beta 2-integrin alpha subunit.";
RL   Gene 171:291-294(1996).
RN   [4]
RP   INTERACTION WITH VCAM1.
RX   MEDLINE=99059842; PubMed=9841932;
RA   Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.,
RA   Hoffman P.A., Staunton D.E., Bochner B.S.;
RT   "alphadbeta2 integrin is expressed on human eosinophils and functions
RT   as an alternative ligand for vascular cell adhesion molecule 1
RT   (VCAM-1).";
RL   J. Exp. Med. 188:2187-2191(1998).
RN   [5]
RP   INTERACTION WITH VCAM1.
RX   MEDLINE=99370002; PubMed=10438935;
RA   Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
RA   Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
RT   "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a
RT   binding interface between I domain and VCAM-1.";
RL   J. Immunol. 163:1984-1990(1999).
CC   -!- FUNCTION: INTEGRIN ALPHA-D/BETA-2 IS A RECEPTOR FOR ICAM3 AND
CC   VCAM1. MAY PLAY A ROLE IN THE ATHEROSCLEROTIC PROCESS SUCH AS
CC   CLEARING LIPOPROTEINS FROM PLAQUES AND IN PHAGOCYTOSIS OF BLOOD-

```
CC       BORNE PATHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES
CC       FROM THE BLOOD.
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D
CC       ASSOCIATES WITH BETA-2.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED MODERATELY ON MYELOMONOCYTIC CELL
CC       LINES AND SUBSETS OF PERIPHERAL BLOOD LEUKOCYTES AND STRONGLY ON
CC       TISSUE-SPECIALIZED CELLS, INCLUDING MACROPHAGES FOAM CELLS WITHIN
CC       ATHEROSCLEROTIC PLAQUES, AND ON SPLENIC RED PULP MACROPHAGES.
CC   -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS
CC       WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
CC   -!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
CC   -!- SIMILARITY: Contains 1 VWFA domain.
CC   -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC       ---------------------------------------------------------------------------
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC       the European Bioinformatics Institute. There are no restrictions on its
CC       use by non-profit institutions as long as its content is in no way
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CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
CC       ---------------------------------------------------------------------------
DR   EMBL; U37028; AAB38547.1; -.
DR   EMBL; U40274; AAB60634.1; -.
DR   EMBL; U40275; AAB60635.1; -.
DR   EMBL; U40276; AAB60636.1; -.
DR   EMBL; U40277; AAB60637.1; -.
DR   EMBL; U40279; AAB60638.1; -.
DR   EMBL; U40278; AAB60638.1; JOINED.
DR   EMBL; AF187881; AAF62875.1; -.
DR   HSSP; P11215; 1A8X.
DR   Genew; HGNC:6146; ITGAD.
DR   MIM; 602453; -.
DR   GO; GO:0008305; C:integrin complex; TAS.
DR   GO; GO:0004895; F:cell adhesion receptor activity; TAS.
DR   GO; GO:0016337; P:cell-cell adhesion; NAS.
DR   GO; GO:0007160; P:cell-matrix adhesion; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR000413; Integrin_alpha.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF01839; FG-GAP; 3.
DR   Pfam; PF00357; Integrin_A; 1.
DR   Pfam; PF00092; vwa; 1.
DR   PRINTS; PR01185; INTEGRINA.
DR   PRINTS; PR00453; VWFADOMAIN.
DR   SMART; SM00191; Int_alpha; 4.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR   PROSITE; PS50234; VWFA; 1.
KW   Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW   Signal; Repeat; Calcium;
KW   Magnesium.
FT   SIGNAL          1     17
FT   CHAIN          18   1162
FT   DOMAIN        101   1100       INTEGRIN ALPHA-D.
FT   TRANSMEM     1101   1124       POTENTIAL.
FT   DOMAIN       1125   1162       CYTOPLASMIC (POTENTIAL).
FT   REPEAT         32     85
FT   REPEAT          ?      ?
FT   DOMAIN        150    332       VWFA.
FT   REPEAT        350    400       FG-GAP 3.
FT   REPEAT        401    452       FG-GAP 4.
FT   REPEAT        454    516       FG-GAP 5.
FT   REPEAT        518    576       FG-GAP 6.
FT   REPEAT        581    633       FG-GAP 7.
FT   REPEAT        465    473       FG-GAP 1.
FT   CA_BIND       530    538       POTENTIAL.
FT   CA_BIND       593    601       POTENTIAL.
FT   SITE         1127   1131       GFFKR MOTIF.
FT   DISULFID       67     74       BY SIMILARITY.
FT   DISULFID      106    124       BY SIMILARITY.
FT   DISULFID      655    710       BY SIMILARITY.
FT   DISULFID      769    775       BY SIMILARITY.
FT   DISULFID      846    861       BY SIMILARITY.
FT   DISULFID      994   1018       BY SIMILARITY.
FT   DISULFID     1023   1028       BY SIMILARITY.
FT   CARBOHYD       59     59       N-LINKED (GLCNAC...) (POTENTIAL).
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FT   CARBOHYD      691    691       N-LINKED (GLCNAC...) (POTENTIAL).
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FT   CARBOHYD      957    957       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     1046   1046       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT      500    500       MISSING (IN REF. 2).
FT   CONFLICT      515    515       GHPW -> ATP (IN REF. 2).
FT   CONFLICT      518    518       L -> V (IN REF. 2).
FT   CONFLICT      825    825       V -> A (IN REF. 2).
FT   SEQUENCE   1162 AA;  126885 MW;  F296A1A3545D77D CRC64;
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Query Match 100.0%; Score 5987; DB 1; Length 1162;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TFGTVLLLSVLASYHGFRLDVEEPTIFQEDAGGFGQSVVQFGGSRLVVGAPLEVVAANQT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 TFGTVLLLSVLASYHGFRLDVEEPTIFQEDAGGFGQSVVQFGGSRLVVGAPLEVVAANQT 61

Qy     61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK 121

Qy    121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMGQFE 181

Qy    181 GTDTLFALMQYSNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTATGILTVVTQLFHH 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 GTDTLFALMQYSNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTATGILTVVTQLFHH 241

Qy    241 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELN 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELN 301

Qy    301 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM 360
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Db    302 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM 361

Qy    361 DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQNLVL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQNLVL 421

Qy    421 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILIGAPH 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILIGAPH 481

Qy    481 YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI 541

Qy    541 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD 601

Qy    601 LAVGARGQVLLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    602 LAVGARGQVLLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS 661

Qy    661 SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCV 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    662 SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCV 721

Qy    721 EDVSPIILHLNFSLVREPIPSPQNLRPVLAVSSQCLFTASLPFKNCGQDGLCEGDLGV 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 EDVSPIILHLNFSLVREPIPSPQNLRPVLAVSSQCLFTASLPFKNCGQDGLCEGDLGV 780
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```
                    GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        August 26, 2003, 10:24:28 ; Search time 91 Seconds
                                            (without alignments)
                                            2025.072 Million cell updates/sec

Title:         US-09-891-943-2
Perfect score: 5987
Sequence:      1 TFGTVLLLSVLASYHGFNLD..........DTATFSGDDFSCVAPNVPLS 1161

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
Searched:      1107863 seqs, 15872673 residues

Total number of hits satisfying chosen parameters:        1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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              24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Result                    %      Query
No.    Score  Match  Length   DB    ID           Description
 1     5987   100.0   1161    16   AAR78166     Human beta-2 integ
 2     5987   100.0   1161    18   AAW23049     Human beta 2 integ
 3     5987   100.0   1161    19   AAW72825     Human alpha-d. Ho
 4     5987   100.0   1161    19   AAW57491     Human beta2 integr
 5     5987   100.0   1161    21   AAB07359     Human alpha_d clon
 6     5987   100.0   1161    23   ABG61468     Human alpha2_integr
 7     5981    99.9   1161    19   AAW65089     Human Beta-integri
 8     5981    99.9   1161    20   AAW73342     Human alphad prote
 9     5971.5  99.7   1161    18   AAW23064     Human beta 2 integ
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ALIGNMENTS

```
RESULT 1
AAR78166
XX
ID    AAR78166 standard; Protein; 1161 PA.
XX
AC    AAR78166;
XX
DT    28-DEC-1995  (first entry)
XX
DE    Human beta-2 integrin alpha-d.
XX
KW    Beta-2 integrin alpha-d subunit; anti-inflammatory; arteriosclerosis;
KW    inflammatory bowel disease; asthma.
OS    Homo sapiens.
XX
FH    Key            Location/Qualifiers
FH
FT    Domain         17..1108
FT                   /note= "extracellular domain"
FT    Region         150..352
FT                   /note= "this region is homologous to the insert
FT                   common to Chila,b,c and may be a site for
FT                   interaction with ICAM family proteins"
FT    Binding-site   465..474
FT                   /note= "putative cation binding site"
FT    Binding-site   518..527
FT                   /note= "putative cation binding site"
FT    Binding-site   592..600
FT                   /note= "putative cation binding site"
FT    Region         1109..1128
FT                   /note= "transmembrane region"
FT    Domain         1129..1161
FT                   /note= "cytoplasmic domain"
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10   5971.5   99.7   1161   19   AAW72837    Human alpha-d deri
11   5971.5   99.7   1161   20   AAW65106    Human Beta-integri
12   5971.5   99.7   1161   20   AAW73343    Human alphad integ
13   5971.5   99.7   1161   21   AAB07376    Human alpha_d prot
14   5971.5   99.7   1161   23   ABG61485    Human Beta2_integr
15   5971.5   99.7   1161   18   AAW23062    Rat beta 2 integri
16   4403.5   73.6   1161   19   AAW72824    Rat alpha-d #1. R
17   4403.5   73.6   1161   21   AAW6C004    Rat alpha d polype
18   4403.5   73.6   1161   23   AAB07374    Rat alpha_d protei
19   4403.5   73.6   1161   21   AAW65104    Rat alpha d integri
20   4397.5   73.5   1161   20   AAB61483    Rat Beta2_integrin
21   4397.5   73.5   1161   19   AAW65104    Rat beta-integrin
22   4397.5   73.4   1161   16   AAW73345    Rat alphad protein
23   4395.5   73.4   1161   19   AAR78169    Rat alpha-d subuni
24   4365.5   72.9   1161   18   AAW23059    Rat beta 2 compos
25   4364.5   72.9   1161   19   AAW65101    Rat beta 2 integri
26   4364.5   72.9   1161   16   AAW60001    Rat alpha-d #2. R
27   4364.5   72.9   1161   20   AAW73344    Rat alpha d polype
28   4364.5   72.9   1161   21   AAB07371    Rat alphad partia
29   4364.5   72.9   1161   23   ABG61480    Rat Beta2_integrin
30   4364.5   72.9   1161   23   AAW23061    Rat alpha-d #2. R
31   4305.0   71.9   1161   18   AAW23061    Mouse beta 2 inte
32   4305.0   71.9   1161   19   AAW72836    Mouse alpha-d #2.
33   4305.0   71.9   1161   19   AAW65103    Mouse beta-integri
34   4305.0   71.9   1161   20   AAW60003    Mouse alpha d poly
35   4305.0   71.9   1161   21   AAB07373    Mouse alphad prote
36   4305.0   71.9   1161   19   AAW73347    Mouse alpha d integr
37   4305.0   71.9   1161   23   ABG61482    Mouse Beta2_integr
38   4303.0   71.9   1161   16   AAR78168    Mouse alpha-d subu
39   4278.5   71.5   1161   16   AAR78167    Mouse alpha-d subu
40   4278.5   71.5   1161   18   AAW23060    Mouse beta 2 integ
41   4278.5   71.5   1161   19   AAW72835    Mouse alpha-d #1.
42   4278.5   71.5   1161   19   AAW65102    Mouse beta-integri
43   4278.5   71.5   1161   20   AAW60002    Mouse alpha d poly
44   4278.5   71.5   1161   19   AAW73346    Mouse alphad prote
45   4278.5   71.5   1161   21   AAB07372    Mouse alpha_d prot
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PN   WO9517412-A1.
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PD   29-JUN-1995.
XX
PF   21-DEC-1994;                94WO-US14832.
XX
PR   05-AUG-1994;                94US-0286889.
PR   23-DEC-1993;                93US-0173497.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Gallatin WM, Van Der Vieren M;
XX
DR   WPI; 1995-240603/31.
DR   N-PSDB; AAQ91712.
XX
PT   Alpha sub-unit polypeptide of human beta 2 integrin - used to
PT   identify potential antiinflammatory agents, for the treatment of
PT   graft arteriosclerosis, inflammatory bowel disease, asthma, etc.
XX
PS   Claim 7; Page 82-87; 172pp; English.
XX
CC   A probe based on a partial cDNA clone (given in AAQ91727) of canine
CC   alpha-TM1 was used to screen a human spleen cDNA library to identify
CC   clone 19A2 encoding the beta-1 integrin alpha-subunit, alpha-d.
CC   The cDNA was manipulated to allow expression of recombinant alpha-d
CC   subunit in COS and CHO cells.
XX
SQ   Sequence    1161 AA;

Query Match             100.0%;  Score 5997;  DB 16;  Length 1161;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1161;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 TFGTVLLLSVLASYHGFNLDVEEPTIFQEDAGGFGQSVVQFGGSRLVVGAPLEVVAANQT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TFGTVLLLSVLASYHGFNLDVEEPTIFQEDAGGFGQSVVQFGGSRLVVGAPLEVVAANQT 60

Qy     61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGTLAAASTNGSRLLACGPTLHRVCGENSYSK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GRLYDCAAATGMCQPIPLHIRPEAVNMSLGTLAAASTNGSRLLACGPTLHRVCGENSYSK 120

Qy    121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMQQFE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDQNDFNQMKGFVQAVMQQFE 180

Qy    181 GTDTLFALMQYSNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTARGILTVVTQLFHH 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTDTLFALMQYSNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTARGILTVVTQLFHH 240

Qy    241 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELN 300
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Db    241 KNGARKSAKKILIVITDGQKYKDPLEYSDVIPQAEKAGIIRYAIGVGHAFQGPTARQELN 300

Qy    301 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM 360

Qy    361 DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQNLVL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQNLVL 420

Qy    421 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILIGAPH 480
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Db    421 GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILIGAPH 480

Qy    481 YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI 540

Qy    541 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQGLMD 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQGLMD 600

Qy    601 LAVGARGQVLLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 LAVGARGQVLLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS 660

Qy    661 SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCV 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCV 720

Qy    721 EDVVSPIILHLNFSLVREPIPSPQNLRPVLAVGSQDLFTASLPFEKNCGQDGLCEGDLGV 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 EDVVSPIILHLNFSLVREPIPSPQNLRPVLAVGSQDLFTASLPFEKNCGQDGLCEGDLGV 780

Qy    781 TLSFSGLQTLTVGSSLELNVIVTWNAGEDSYGTVVSLYPAGLSHRRVSGAQKQPHQSA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TLSFSGLQTLTVGSSLELNVIVTWNAGEDSYGTVVSLYPAGLSHRRVSGAQKQPHQSA 840

Qy    841 LRLACETVPTEDEGLRSSRSCSVNHPIFHEGSNGTFIVTFDVSYKATLGDRMLMRASASSE 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 LRLACETVPTEDEGLRSSRSCSVNHPIFHEGSNGTFIVTFDVSYKATLGDRMLMRASASSE 900

Qy    901 NNKASSSKATFQLELPVKYAVYTMISRQEESTKYFNFATSDEKKMKEAEHRYRVNNLSQR 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 NNKASSSKATFQLELPVKYAVYTMISRQEESTKYFNFATSDEKKMKEAEHRYRVNNLSQR 960

Qy    961 DLAISINFWVPVLLNGVAVWDVMEARSQSLPCVSERKPPQHSDFLTQISRSSPMLDCSIA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 DLAISINFWVPVLLNGVAVWDVMEARSQSLPCVSERKPPQHSDFLTQISRSSPMLDCSIA 1020

Qy   1021 DCLQFRCDVPSFSVQEELDFTLKGNLSFGWVRETLQKKVLLVVSVAEITFDTSVYSQLPG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 DCLQFRCDVPSFSVQEELDFTLKGNLSFGWVRETLQKKVLLVVSVAEITFDTSVYSQLPG 1080

Qy   1081 EAFMRAQMEMVLEEDSVYNAIPIIMGSSVGALLLLALITAVLYKLGFFKRHYKEMLEDKP 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 EAFMRAQMEMVLEEDSVYNAIPIIMGSSVGALLLLALITAVLYKLGFFKRHYKEMLEDKP 1140

Qy   1141 EDTATFSGDDFSCVAPNVPLS 1161
          |||||||||||||||||||||
Db   1141 EDTATFSGDDFSCVAPNVPLS 1161
```

RESULT 2
AAW23049

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ID   AAW23049 standard; Protein; 1161 AA.
XX
AC   AAW23049;
XX
DT   24-FEB-1998 (first entry)
XX
DE   Human beta 2 integrin alpha d subunit.
XX
KW   Beta 2 integrin alpha d subunit; human; cell migration;
KW   cell adhesion; phagocytosis; diabetes; atherosclerosis;
KW   multiple sclerosis; asthma; psoriasis; lung inflammation;
KW   acute respiratory distress syndrome; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
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FT   Domain           150..352
FT                    /note= "region homologous to the I (insertion)
FT                    domain common to CD11a, CD11b and CD11c"
XX
```

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:37:23 ; Search time 71 Seconds
(without alignments)
2157.853 Million cell updates/sec

Title: US-09-891-943-2
Perfect score: 5987
Sequence: 1 TFGTVLLLSVLASYHGFNLD.........DTATFSGDDFSCVAPNVPLS 1161

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 13196171B residues

Total number of hits satisfying chosen parameters: 497079

Post-processing: Minimum Match 0%
Minimum DB seq length: 0
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Database : Published Applications AA:*
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Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	5987	100.0	1161	11	US-09-891-943-2	Sequence 2, Appli
3	5971.5	99.7	1161	9	US-09-350-259-99	Sequence 99, Appl
4	5971.5	99.7	1161	11	US-09-891-943-99	Sequence 99, Appl
5	4403.5	73.6	1161	9	US-09-350-259-55	Sequence 55, Appl
6	4403.5	73.6	1161	11	US-09-891-943-55	Sequence 55, Appl
7	4364.5	72.9	1151	9	US-09-350-259-37	Sequence 37, Appl
8	4364.5	72.9	1151	11	US-09-891-943-37	Sequence 37, Appl
9	4305.5	71.9	1161	9	US-09-350-259-53	Sequence 53, Appl
10	4305.5	71.9	1161	11	US-09-891-943-53	Sequence 53, Appl
11	4278.5	71.5	1155	9	US-09-350-259-46	Sequence 46, Appl
12	4278.5	71.5	1155	11	US-09-891-943-46	Sequence 46, Appl
13	3746	62.6	1163	9	US-09-350-259-4	Sequence 4, Appli
14	3746	62.6	1163	11	US-09-891-943-4	Sequence 4, Appli
15	3455	57.7	1153	9	US-09-350-259-3	Sequence 3, Appli
16	3455	57.7	1153	11	US-09-902-481A-1	Sequence 1, Appli
17	3455	57.7	1153	11	US-09-891-943-3	Sequence 3, Appli
18	3455	57.7	1153	15	US-10-144-259-30	Sequence 30, Appl
19	3455	57.7	1153	15	US-10-207-655-176	Sequence 176, App
20	3439.5	57.4	1152	10	US-09-945-265-4	Sequence 4, Appli
21	3417	57.1	1137	11	US-09-902-481A-6	Sequence 6, Appli
22	3411	57.0	1137	11	US-09-902-481A-5	Sequence 5, Appli
23	3401	56.8	1137	11	US-09-902-481A-4	Sequence 4, Appli
24	3388	56.6	1137	11	US-09-902-481A-3	Sequence 3, Appli
25	1833	30.6	494	9	US-09-350-259-103	Sequence 103, App
26	1833	30.6	494	11	US-09-891-943-103	Sequence 103, App
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45	610.5	10.2	199	15	US-10-066-551-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/09350259
; Patent No. US2002006200BA1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: NO. US2002006200BA1e1 Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US:09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-2

Query Match 100.0%; Score 5987; DB 9; Length 1161;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1161 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              Copyright (c) 1993 - 2003  Compugen Ltd.

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              Pred. No. is the number of results predicted by chance to have a
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4	5981	99.9	1161	1	US-08-286-889-2	Sequence 2, Appli
5	5981	99.9	1161	1	US-08-485-618-2	Sequence 2, Appli
6	5981	99.9	1161	1	US-08-362-652-2	Sequence 2, Appli
7	5981	99.9	1161	2	US-08-605-672-2	Sequence 2, Appli
8	5981	99.9	1161	2	US-08-482-293A-2	Sequence 2, Appli
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; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
;  TITLE OF INVENTION: No. 62513956el Human 2
;  FILE REFERENCE: 27866/35004
;  CURRENT APPLICATION NUMBER: US/09/193,043
;  CURRENT FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
;  EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
;  EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
;  EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
;  EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 2
;  LENGTH: 1161
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-193-043-2

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Qy   1021  DCLQFRCDVPSFSVQEELDFTLKGNLSFGWVRETLQKKVLVVSVAEITFDTSVYSQLPGQ  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  DCLQFRCDVPSFSVQEELDFTLKGNLSFGWVRETLQKKVLVVSVAEITFDTSVYSQLPGQ  1080

Qy   1081  EAFMRAQMEMVLEEDEVTYNAIPIIMGSSVGALLLLALITATLYKLGFFKRHYKEMLEDKP  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  EAFMRAQMEMVLEEDEVTYNAIPIIMGSSVGALLLLALITATLYKLGFFKRHYKEMLEDKP  1140

Qy   1141  EDTATFSGDDFSCVAPNVPLS  1161
           |||||||||||||||||||||
Db   1141  EDTATFSGDDFSCVAPNVPLS  1161
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Qy      1  TFGTVLLLSVLASYHGFNDLVEEPTIFQEDAGGFGQOSVVQFGGSRLVVGAPLEVVAANQT  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  TFGTVLLLSVLASYHGFNDLVEEPTIFQEDAGGFGQOSVVQFGGSRLVVGAPLEVVAANQT  60

Qy     61  GRLYDCAAATGMCQPIPLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GRLYDCAAATGMCQPIPLHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSK  120

Qy    121  GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDCNDFNQMKGFVQAVMGQFE  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GSCLLLGSRWEIIQTVPDATPECPHQEMDIVFLIDGSGSIDCNDFNQMKGFVQAVMGQFE  180

Qy    181  GTDTLFALMQYSNLLK IHFFTTQFRTSFSQQSLVDPIVQLKGLTFTATGILTVVTQLFHH  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GTDTLFALMQYSNLLK IHFFTTQFRTSFSQQSLVDPIVQLKGLTFTATGILTVVTQLFHH  240

Qy    241  KNGARKSAKKILIVITDGQKYKDPLEYSDVIFQPEAKAGIIRYAIGVGHAFQGGPTARQELN  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  KNGARKSAKKILIVITDGQKYKDPLEYSDVIFQPEAKAGIIRYAIGVGHAFQGGPTARQELN  300

Qy    301  TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  TISSAPPQDHVFKVDNFAALGSIQKQLQEKIYAVEGTQSRASSSFQHEMSQEGFSTALTM  360

Qy    361  DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQNLVL  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  DGLFLGAVGSFSWSGGAFLYPPNMSPTFINMSQENVDMRDSYLGYSTELALWKGVQNLVL  420

Qy    421  GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILIGAPH  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GAPRYQHTGKAVIFTQVSRQWRKKAEVTGTQIGSYFGASLCSVDVDSDGSTDLILIGAPH  480

Qy    481  YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  YYEQTRGGQVSVCPLPRGQRVQWQCDAVLRGEQGHPWGRFGAALTVLGDVNEDKLIDVAI  540

Qy    541  GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GAPGEQENRGAVYLFHGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMD  600

Qy    601  LAVGARGQVLLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  LAVGARGQVLLLRSLPVLKVGVAMRFSPVEVAKAVYRCWEEKPSALEAGDATVCLTIQKS  660

Qy    661  SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCV  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  SLDQLGDIQSSVRFDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCV  720

Qy    721  EDVVSPIILHLHNFSLVREPIPSPQNLRPVLAVGSQDLFTASLPFEKNCGQDGLCEGDLGV  780
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